



Primary structure of human nonmuscle-type cofilin
(AC: P23528)

MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNIILE
EGKEILVGDV
GQTVDDPYAT FVKMLPDKDC RYALYDATYE TKESKKEDLV FIFWAPESAP
LKSKMIYASS
KDAIKKKLTG IKHELQANCY EEVKDRCTLA EKLGGSAVIS LEGKPL

The underlined portions are the sites analyzed for
sequence by MS and MS/MS.

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn

5 10 15

Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg

20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile

35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val

50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

65 70 75 80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys

85 90 95

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys

100 105 110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu

115 120 125

Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys

130 135 140

Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser

145 150 155 160

Leu Glu Gly Lys Pro Leu SEQ ID NO: 1

165

Fig. 1

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cDNA of human placental nonmuscle-type cofilin
(AC: D00682)

atggcctccg gtgtggctgt ctctgatgg gtcataagg tgttcaacga catgaagggtg 60
cgtaagtcct caacgccaga ggaggtgaag aagcgcaaga aggcgggtgct ctctgcctg 120
agtgaggaca agaagaacat catcctggag gagggcaagg agatcctggt gggcgatgtg 180
ggccagactg tcgacgatcc ctacgccacc ttgtcaaga tgctgccaga taaggactgc 240
cgctatgccc tctatgatgc aacctatgag accaaggaga gcaagaagga ggatctgggtg 300
tttatcttct gggccccga gctgcgccc cttaagagca aatgattta tgccagctcc 360
aaggacgcca tcaagaagaa gctgacagg atcaagcatg aattgcaagc aaactgctac 420
gaggagggtca aggaccgctg caccctggca gagaagctgg ggggcagtgc ggtcatctcc 480
ctggagggca agcctttgtg a SEQ ID NO: 2 501

The underlined portions are the sites where two
oligomers were synthesized as primers.

Fig. 2

Alignment of the base sequences for nonmuscle-type cofilin
derived from human placenta (upper)
and from human S6 cells (lower).

		10	20	30	40	50	
Placental cDNA	1	ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG		
TGTTCAACGA	50						
S6 cDNA	1	ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG		
TGTTCAACGA	50						
		60	70	80	90	100	
Placental cDNA	51	CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA	GGAGGTGAAG		
AAGCGCAAGA	100						
S6 cDNA	51	CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA			
GGAGGTGAAG	100						
		110	120	130	140	150	
Placental cDNA	101	AGGCGGTGCT	CTTCTGCCTG	AGTGAGGACA	AGAAGAACAT		
CATCCTGGAG	150						
S6 cDNA	101	AGGCGGTGCT	CTTCTGCCTG	AGTGAGGACA			
AGAAGAACAT	150						
		160	170	180	190	200	
Placental cDNA	151	GAGGGCAAGG	AGATCCTGGT	GGGCGATGTG	GGCCAGACTG		
TCGACGATCC	200						
S6 cDNA	151	GAGGGCAAGG	AGATCCTGGT	GGGCGATGTG			
GGCCAGACTG	200						
		210	220	230	240	250	
Placental cDNA	201	CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC		
CGCTATGCCC	250						
S6 cDNA	201	CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC		
CGCTATGCCC	250						
		260	270	280	290	300	
Placental cDNA	251	TCTATGATGC	AACCTATGAG	ACCAAGGAGA	GCAAGAAGGA		
GGATCTGGTG	300						
S6 cDNA	251	TCTATGATGC	AACCTATGAG	ACCAAGGAGA			
GCAAGAAGGA	300						
		310	320	330	340	350	
Placental cDNA	301	TTTATCTTCT	GGGCCCCCGA	GTCTGCGCCC	CTTAAGAGCA		
AAATGATTTA	350						
S6 cDNA	301	TTTATCTTCT	GGGCCCCCGA	GTCTGCGCCC	CTTAAGAGCA		
AAATGATTTA	350						
		360	370	380	390	400	
Placental cDNA	351	TGCCAGCTCC	AAGGACGCCA	TCAAGAAGAA	GCTGACAGGG		
ATCAAGCATG	400						
S6 cDNA	351	TGCCAGCTCC	AAGGACGCCA	TCAAGAAGAA			
GCTGACAGGG	400						
		410	420	430	440	450	
Placental cDNA	401	AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA	AGGACCGCTG		
CACCCTGGCA	450						
S6 cDNA	401	AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA			
AGGACCGCTG	450						
		460	470	480	490	500	
Placental cDNA	451	GAGAAGCTGG	GGGGCAGTGC	GGTCATCTCC	CTGGAGGGCA		
AGCCTTTGTG	500						
S6 cDNA	451	GAGAAGCTGG	GGGGCAGTGC	GGTCATCTCC			
CTGGAGGGCA	500						
		510	520	530	540	550	
Placental cDNA	501	A.....	SEQ ID NO: 2
S6 cDNA	501	A.....	SEQ ID NO: 8

The two bases that differ between the two sequences are marked
by shadowing and are both due to silent mutation.

Fig. 3